

OIKE

## RAW SEQUENCE LISTING

DATE: 09/21/2001

PATENT APPLICATION: US/09/944,807

TIME: 20:48:14

Input Set : A:\Sequence Listing 1\_1144.txt

Output Set: N:\CRF3\09212001\I944807.raw

3 <110> APPLICANT: Boehringer Ingelheim Pharma KG  
 5 <120> TITLE OF INVENTION: Method for identifying substances which positively  
 6 influence inflammatory conditions of chronic  
 7 inflammatory airway diseases  
 9 <130> FILE REFERENCE: 082\_00n  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/944,807  
 C--> 12 <141> CURRENT FILING DATE: 2001-08-31  
 14 <150> PRIOR APPLICATION NUMBER: UK 0021484.1  
 15 <151> PRIOR FILING DATE: 2000-09-01  
 17 <160> NUMBER OF SEQ ID NOS: 24  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1910  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <400> SEQUENCE: 1  
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 28 gaatgaatat gaagaagtgt cctatgagtc tgctggctac actgttctgc ggatcctccc 120  
 29 attggtggtg cttgggggtca cctttgtcct cggggctcctg ggcaatgggc ttgtgatctg 180  
 30 ggtggctgga ttccggatga cacgcacagt caccaccatc tgttacctga acctggccct 240  
 31 ggctgacttt tctttcacgg ccacattacc attcctcatt gtctccatgg ccattgggaga 300  
 32 aaaatggcct tttggctggt tcctgtgtaa gttaattcac atcgtgggtg acatcaacct 360  
 33 ctttggaagt gtcttcttga ttggtttcat tgcaactggac cgctgcattt gtgtcctgca 420  
 34 tccagtctgg gcccagaacc accgcactgt gagtctggcc atgaaggtga tcgtcggacc 480  
 35 ttggattctt gctctagtcc ttaccttgcc agttttcctc tttttgacta cagtaactat 540  
 36 tccaaatggg gacacatact gtactttcaa ctttgcaccc tgggggtggca cccctgagga 600  
 37 gaggctgaag gtggccatta ccattgctgac agccagaggg attatccggt ttgtcattgg 660  
 38 ctttagcttg cggatgtcca ttgttgccat ctgctatggg ctcatcgag ccaagatcca 720  
 39 caaaaagggc atgattaaat ccagccgtcc cttacgggtc ctactgctg tgggtggcttc 780  
 40 tttcttcac tgttggtttc cttttcaact gggtgcccct ctgggcaccg tctggctcaa 840  
 41 agagatgttg ttctatggca agtacaaaat cattgacatc ctggttaacc caacgagctc 900  
 42 cctggccttc ttcaacagct gcctcaaccc catgctttac gtctttgtgg gccaaagactt 960  
 43 ccgagagaga ctgatccact ccctgcccac cagtctggag agggccctgt ctgaggactc 1020  
 44 agccccaact aatgacacgg ctgccaatte tgcttcacct cctgcagaga ctgagttaca 1080  
 45 ggcaatgtga ggatgggggc agggatattt tgagttctgt tcatcctacc ctaatgccag 1140  
 46 ttccagcttc atctaccctt gagtcatatt gaggcattca aggatgcaca gctcaagtat 1200  
 47 ttattcagga aaaatgcttt tgtgtccctg atttggggct aagaaataga cagtcaggct 1260  
 48 actaaaatat tagtgttatt ttttgttttt tgacttctgc ctataccctg gggtaagtgg 1320  
 49 agttgggaaa tacaagaaga gaaagaccgg tggggatttg taagacttag atgagatagt 1380  
 50 gcataataag ggggaagactt taaagtataa agtaaaatgt ttgctgtagg ttttttatag 1440  
 51 ctattaaaaa aatcagatt atggaagttt tcttctattt ttagtttgct aagagttttc 1500  
 52 tgttttcttt tcttacattg tgagtggact ttgcatttta tcaaatgcat tttctacatg 1560  
 53 tattaagatg gtcattatct tcttctctt ttagttaaatt cattataaat aatgttctatt 1620  
 54 aagttctgaa gttaaaacta ctcttgaatt cctggaataa accacactta gtcctgatgt 1680  
 55 actttaaata tttatatctc acaggagttg gttagaattt ctgtgtttat gtttatatac 1740  
 56 tgttatattca ctttttctac tatccttgct aagttttcat agaaaataag gaacaaagag 1800  
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ENTERED

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58 tgttatatct ttattaaata ttcagaaaaa ttcaccagtg aaaaaaaaaa      1910
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 351
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 2
67 Met Glu Thr Asn Phe Ser Thr Pro Leu Asn Glu Tyr Glu Glu Val Ser
68   1           5           10           15
70 Tyr Glu Ser Ala Gly Tyr Thr Val Leu Arg Ile Leu Pro Leu Val Val
71           20           25           30
73 Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile
74           35           40           45
76 Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr
77           50           55           60
79 Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe
80           65           70           75           80
82 Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe
83           85           90           95
85 Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser
86           100          105          110
88 Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
89           115          120          125
91 His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys
92           130          135          140
94 Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val
95           145          150          155          160
97 Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys
98           165          170          175
100 Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys
101           180          185          190
103 Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile
104           195          200          205
106 Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile
107           210          215          220
109 Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu
110           225          230          235          240
112 Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
113           245          250          255
115 Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu
116           260          265          270
118 Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser
119           275          280          285
121 Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe
122           290          295          300
124 Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser
125           305          310          315          320
127 Leu Glu Arg Ala Leu Ser Glu Asp Ser Ala Pro Thr Asn Asp Thr Ala
128           325          330          335
130 Ala Asn Ser Ala Ser Pro Pro Ala Glu Thr Glu Leu Gln Ala Met

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131          340          345          350
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 2433
136 <212> TYPE: DNA
137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 3
140 cagccgcggc ccatggagcc cgcgcggccc gcccccgccc gcctcggggc gctgctctgc 60
141 ctgctgctcg ccgcgtcctg cgcctgggtc ggagtgccgg gtgaggagga gctgcagggtg 120
142 attcagcctg acaagtccgt atcagttgca gctggagagt cggccattct gcactgcact 180
143 gtgacctccc tgatccctgt ggggcccata cagtgggttc gaggagctgg accagcccgg 240
144 gaattaatct acaatcaaaa agaaggccac tccccccggg taacaactgt ttcagagtcc 300
145 acaaagagag aaaacatgga cttttccatc agcatcagta acatcacccc agcagatgcc 360
146 ggcacctact actgtgtgaa gttccggaaa gggagccctg acacggagtt taagtctgga 420
147 gcaggcactg agctgtctgt gcgtgccaaa cctctgccc ccgtgggtatc gggccctgcg 480
148 gcgagggcca cacctcagca cacagtgagc ttcacctgcg agtcccacgg cttctcacc 540
149 agagacatca cctgaaatg gttcaaaaat gggaaatgagc tctcagactt ccagaccaac 600
150 gtggaccccg taggagagag cgtgtcctac agcatccaca gcacagccaa ggtggtgctg 660
151 acccgcgagg acgttcactc tcaagtcate tgcgaggtgg ccacgtcac cttgcagggg 720
152 gacctcttc gtgggactgc caacttgtct gagaccatcc gagttccacc caccttgga 780
153 gttactcaac agcccgtag ggcagagaa cagggtgaatg tcacctgcca ggtgaggaag 840
154 ttctaccccc agagactaca gctgacctgg ttggagaatg gaaacgtgtc ccggacagaa 900
155 acggcctcaa ccgttacaga gaacaaggat ggtacctaca actggatgag ctggctcctg 960
156 gtgaatgtat ctgccacag ggatgatgtg aagctcacct gccagggtga gcatgacggg 1020
157 cagccagcgg tcagcaaaag ccatgacctg aaggtctcag cccacccgaa ggagcagggc 1080
158 tcaaataacc ccgctgagaa cactggatct aatgaacgga acatctatat tgtggtgggt 1140
159 gtggtgtgca cttgtctggt ggcctactg atggcggccc tctacctcgt ccgaatcaga 1200
160 cagaagaaag cccagggctc cacttcttct acaaggttgc atgagcccga gaagaatgcc 1260
161 agagaaataa cacaggacac aatgatata acatatgcag acctgaacct gcccaagggg 1320
162 aagaagcctg ctccccaggg tgcggagccc aacaaccaca cggagtatgc cagcattcag 1380
163 accagcccgc agcccgcgtc ggaggacacc ctacacctat ctgacctgga catggtccac 1440
164 ctcaaccgga cccccaagca gccggccccc aagcctgagc cgtccttctc agagtacgcc 1500
165 agcgtccagg tcccagggaa gtgaatggga ccgtggtttg ctctagcacc catctctacg 1560
166 cgctttcttg tcccacaggg agccgcctg atgagcacag ccaaccaggt tcccggaggg 1620
167 ctggggcggt gcaggctctg ggacccaggg gccagggtgg ctcttctctc cccaccctc 1680
168 cttggctctc cagcacttcc tgggcagcca cggccccctc cccaacatt gccacacacc 1740
169 tggaggctga cgttgccaaa ccagccaggg aaccaacctg ggaagtggcc agaactgcct 1800
170 ggggtccaag aactcttggt cctccgtcca tcacctgtg ggttttgaag accctcgact 1860
171 gcctccccga tgctccgaag cctgatcttc cagggtgggg aggagaaaat cccacctccc 1920
172 ctgacctcca ccacctccac caccaccacc accaccacca ccaccactac caccaccacc 1980
173 caactggggc tagagtgggg aagatttccc ctttagatca aactgcccct tccatggaaa 2040
174 agctggaaaa aaactctgga acccatatcc aggccttggt aggttgctgc caacagtcct 2100
175 ggcctcccc atccctaggc aaagagccat gagtccctga ggaggagagg acccctccca 2160
176 aaggactgga agcaaaaccc tctgtcttct tgggtccctc caagactccc tggggcccaa 2220
177 ctgtgttgct ccaccggac ccatctctcc cttctagacc tgagcttgcc cctccagcta 2280
178 gactaagca acatctcgt gtaagcgcct gtaaattact gtgaaatgtg aaacgtgcaa 2340
179 tcttgaaact gaggtgttag aaaacttgat ctgtggtgtt ttgtttgtt tttttctta 2400
180 aaacaacagc aacgtgaaaa aaaaaaaaaa aaa 2433
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 503

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185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 4
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190   1           5           10           15
192 Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
193           20           25           30
195 Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly
196           35           40           45
198 Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
199           50           55           60
201 Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr
202   65           70           75           80
204 Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
205           85           90           95
207 Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
208           100          105          110
210 Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
211           115          120          125
213 Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
214           130          135          140
216 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
217   145          150          155          160
219 Pro/Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
220           165          170          175
222 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
223           180          185          190
225 Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
226           195          200          205
228 His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
229           210          215          220
231 Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
232   225          230          235          240
234 Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
235           245          250          255
237 Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
238           260          265          270
240 Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
241           275          280          285
243 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
244           290          295          300
246 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
247   305          310          315          320
249 Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
250           325          330          335
252 Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
253           340          345          350
255 Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
256           355          360          365

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258 Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
259      370                      375                      380
261 Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
262 385                      390                      395                      400
264 Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
265                      405                      410                      415
267 Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
268                      420                      425                      430
270 Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
271                      435                      440                      445
273 His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
274                      450                      455                      460
276 Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
277 465                      470                      475                      480
279 Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
280                      485                      490                      495
282 Ser Val Gln Val Pro Arg Lys
283                      500
286 <210> SEQ ID NO: 5
287 <211> LENGTH: 759
288 <212> TYPE: DNA
289 <213> ORGANISM: Homo sapiens
291 <400> SEQUENCE: 5
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294 aagaagcacg gtatgatgac caaacataaa aagtgtttta taattgttgg tgttttaata 180
295 acaactaata ttattactct gatagttaaa ctaactcgag attctcagag tttatgcccc 240
296 tatgattgga ttggtttcca aaacaaatgc tattatttct ctaaagaaga aggagattgg 300
297 aattcaagta aatacaactg ttccactcaa catgccgacc taactataat tgacaacata 360
298 gaagaaatga attttcttag gcggtataaa tgcagttctg atcactggat tggactgaag 420
299 atggcaaaaa atcgaacagg acaatgggta catggagcta catttaccaa atcgtttggc 480
300 atgagaggga gtgaaggatg tgcctacctc agcgatgatg gtgcagcaac agctagatgt 540
301 tacaccgaaa gaaaatggat ttgcaggaaa agaatacact aagttaatgt ctaagataat 600
302 ggggaaaata gaaaataaca ttattaagtg taaaaccagc aaagtacttt ttttaattaaa 660
303 caaagttcga gttttgtacc tgtctgggta attctgctta cgtgtcaggc tacacataaa 720
304 agccacttca aagattggca aaaaaaaaaa aaaaaaaaaa 759
307 <210> SEQ ID NO: 6
308 <211> LENGTH: 149
309 <212> TYPE: PRT
310 <213> ORGANISM: Homo sapiens
312 <400> SEQUENCE: 6
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316 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
317                      20                      25                      30
319 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
320                      35                      40                      45
322 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
323 50                      55                      60

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VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing 1\_1144.txt

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date